

BATCH

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/602,597

DATE: 12/04/2000
TIME: 12:08:25

Input Set : A:\472.app
Output Set: N:\CRF3\12042000\I602597.raw

P.5

ENTERED

4 <110> APPLICANT: Duhl, David
5 Gorman, Susan Wilkie
7 <120> TITLE OF INVENTION: HUMAN CHROMOSOME 15 AND 16 BARDET-BIEDL
8 SYNDROME POLYNUCLEOTIDES AND POLYPEPTIDES AND METHODS OF USE
11 <130> FILE REFERENCE: 200130.472/1568.002
13 <140> CURRENT APPLICATION NUMBER: 09/602,597
14 <141> CURRENT FILING DATE: 2000-06-22
16 <160> NUMBER OF SEQ ID NOS: 12
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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28 agagcgagcg gctctgcggt ggcggttttg ggtggggccc gccgaggtga ggtcgtctcg 180
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34 ctgatgagg tttctcgaca gcaggaaact atagaaaagc aacgaagaga agaagaactg 540
35 aaagaactga aggaatacac aaataacctc aagaagggtg gaattttctc agagaacaa 600
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37 gcgaagctgt tggcaggagc tgtgaagcat aagaactcag agagtggcaa cagtgtgaaa 720
38 agactgaaac cggaccttga gccagatgac aagaatcaag agccctcctc ctgcaagtct 780
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41 agcgaaaggc ccatcaatgc caccggaaag attgtctcct ccactctccg aaccaacacc 960
42 ttcctcgagg ccccttagtt tctccgtccc tacacaggga gctcctccc aagggtatag 1020
43 cggaccgttc atgtgtccta taggcattat gtccctcaaa aaaaaactcc tttgcctgca 1080
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50 gaagagaact gaccaggtta atgaaatgga gcccttccct ggaactaacc agtccctgat 1500
51 gtlgtgtgac taagttaaaga tgaLaaaccc catctgctgg ggggtgtaact tcacaclegg 1560
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57 acacttgcat attgtgacca ttctatttgg gccctctctg tttaatgcat attatacttg 1920
58 tgccttttaac tgtggaactc atttctaacc taaagggtgt gccctagtac ttttcttttg 1980

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Input Set : A:\472.app

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61 aggaqggaga gggagatggt gtggagggct cgaaggacaga gatagacatg agctttgaca 2160
62 acaatctgta ggctctctctg ctttagaata agcatgtacc attctttatc cattccctct 2220
63 attctacat caattgtttt tactttcttg ggtgtgagac tgagtgagac acacacaaaa 2280
64 tgtgttgaca ctgtgatgcc ggcaggcaga gcagctactg actttgaaca tgggcagaga 2340
65 ggcctctgga telcatccag cccactcctt tcccccttcc aqtacagtga cactctggtg 2400
66 cccattggca gatggcgact tccctgcacc cataactgat gctttgtgaa ttcttctctc 2460
67 ttttcagaac tactctgtgc taattgttct gccagtatgy ggcgcatcagc tccatcctga 2520
68 caaacaagac atttaggtaa aactttgtag gcaccttctg cttctctgct tcattgttcc 2580
69 tgtgatagtc ctgttgttat tacagcatgt acccaaaaaca gccctacatt gttacaggag 2640
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73 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2850
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84 20 25 30
85 Glu Lys Val Arg Lys Pro Glu Asp Pro Glu Glu Cys Pro Glu Glu Val
86 35 40 45
87 Tyr Asp Pro Arg Ser Leu Tyr Glu Arg Leu Gln Glu Gln Lys Asp Arg
88 50 55 60
89 Lys Gln Gln Glu Tyr Glu Glu Gln Phe Lys Phe Lys Asn Met Val Arg
90 65 70 75 80
91 Gly Leu Asp Glu Asp Glu Thr Asn Phe Leu Asp Glu Val Ser Arg Gln
92 85 90 95
93 Gln Glu Leu Ile Glu Lys Gln Arg Arg Glu Glu Glu Leu Lys Glu Leu
94 100 105 110
95 Lys Glu Tyr Arg Asn Asn Leu Lys Lys Val Gly Ile Ser Gln Glu Asn
96 115 120 125
97 Lys Lys Glu Val Glu Lys Lys Leu Thr Val Lys Pro Ile Glu Thr Lys
98 130 135 140
99 Asn Lys Phe Ser Gln Ala Lys Leu Leu Ala Gly Ala Val Lys His Lys
100 145 150 155 160
101 Ser Ser Glu Ser Gly Asn Ser Val Lys Arg Leu Lys Pro Asp Pro Glu
102 165 170 175
103 Pro Asp Asp Lys Asn Gln Glu Pro Ser Ser Cys Lys Ser Leu Gly Asn
104 180 185 190
105 Thr Ser Leu Ser Gly Pro Ser Ile His Cys Pro Ser Ala Ala Val Cys
106 195 200 205
107 Ile Gly Ile Leu Pro Gly Leu Gly Ala Tyr Ser Gly Ser Ser Asp Ser
108 210 215 220
109 Glu Ser Ser Ser Asp Ser Glu Gly Thr Ile Asn Ala Thr Gly Lys Ile

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Input Set : A:\472.app

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122 agttagcacg cggaccagca gtcctgcgca gggcgccgaa gcctcggtgt cggcgctgcy      180
123 cccggacctg ggtttcgtgc gctcccgctt cggggcgctc atgctgtctc agctggtgct      240
124 ggggctgctg gtgtgggcgc tgattgcgga caccocgtac cactgtatc cggcctatgg      300
125 ctgggtgatg ttctgtctgt tcttctctgt gctggtgaca atcgtctctt tcaaccteta      360
126 cctgtttcag ctgcacatga agttgtacat ggttccctgg ccactgggtg taatgatctt      420
127 taacatcagc gccaccgttc tctacatcac cgccttcata gcctgctctg cggcagttga      480
128 cctgacatcc ctgaggggca cccggcctta taaccagcgc cgggctgctt cgttctttgc      540
129 gtgtttgggt atgatcgctt atggagtgag tgccttcttc agctaccagg cctggcgagg      600
130 agtaggcagc aatgcggcca ccagtcagat ggtcgccggc tatgcctaaa ccacctgtgc      660
131 cacggccccc tctggggctg aagccgcgcg tgggtcacag agcagggtca cctgcgaaac      720
132 ctgaaagctg ggagccctgc gtggagtcag cccaacaggc actgcatttg ctctctctgt      780
133 cccgtcagac ataatctctc acagcgctaa ggaagcaggg ccaggctggc agcatctctg      840
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136 gggccaccct tctcaccagc ictaaatgca ctaacaagga ctccagacct gcaagccacc      1020
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142 ctaacatcgg tgcctccccg acctgtctga ctaggcacat gggacgcaaa ggaggaggg      1380
143 aagcaagccc ttgcctggcg agttgtcatg tgggttggtg tgactgtttt atttttttta      1440
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157 Val Arg Ser Arg Leu Gly Ala Leu Met Leu Leu Gln Leu Val Leu Gly
158          35          40          45
159 Leu Leu Val Trp Ala Leu Ile Ala Asp Thr Pro Tyr His Leu Tyr Pro
160          50          55          60
161 Ala Tyr Gly Trp Val Met Phe Val Ala Val Phe Leu Trp Leu Val Thr
162 65          70          75          80

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166                               100                              105                              110
167 Val Leu Tyr Ile Thr Ala Phe Ile Ala Cys Ser Ala Ala Val Asp Leu
168                               115                              120                              125
169 Thr Ser Leu Arg Gly Thr Arg Pro Lys Asn Gln Arg Ala Ala Ala Ser
170                               130                              135                              140
171 Phe Phe Ala Cys Leu Val Met Ile Ala Tyr Gly Val Ser Ala Phe Phe
172 145                               150                              155                              160
173 Ser Tyr Gln Ala Trp Arg Gly Val Gly Ser Asn Ala Ala Thr Ser Gln
174                               165                              170                              175
175 Met Ala Gly Gly Tyr Ala Thr Thr Cys Ala Thr Ala Pro Ser Gly Ala
176                               180                              185                              190
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178                               195                              200                              205
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184 <212> TYPE: DNA
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204 cgggccactc caggtcaacc agacagggca cacacatccc cagcccagta tgaatgcaca      1020
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211 gatctttcag gaaaaccagg aggaagggca tgaggagggt ttgaggccct cagccagttc      1440
212 gtgtgctggg gtggagcaac tcagaagagt caggccacac cacttgaata cactcaactt      1500
213 aggaactcctc tgaggcatgt ctctgaggct gcccaacttc caatggctct gggcgttct      1560

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216 tcccaggaca gcacttccat tccctgggtg cctgagatgg tggcagaggc tccagactga 1740
217 gccagagaag ctgtgtgtct gccataacag gcacccctgt ctgagcacag gtgatcctgc 1800
218 tgggaagaggc gtggagtgaa ctctttctcc tcggggccat ccagtgtctc ctgctcttgg 1860
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237 35 40 45
238 Val Cys Gly Asp Ser Ser Ser Gly Lys His Tyr Gly Ile Tyr Ala Cys
239 50 55 60
240 Asn Gly Cys Ser Gly Phe Phe Lys Arg Ser Val Arg Arg Arg Leu Ile
241 65 70 75 80
242 Tyr Arg Cys Gln Val Gly Ala Gly Met Cys Pro Val Asp Lys Ala His
243 85 90 95
244 Arg Asn Gln Cys Gln Ala Cys Arg Leu Lys Lys Cys Leu Gln Ala Gly
245 100 105 110
246 Met Asn Gln Asp Ala Val Gln Asn Glu Arg Gln Pro Arg Ser Thr Ala
247 115 120 125
248 Gln Val His Leu Asp Ser Met Glu Ser Asn Thr Glu Ser Arg Pro Glu
249 130 135 140
250 Ser Leu Val Ala Pro Pro Ala Pro Ala Gly Arg Ser Pro Arg Gly Pro
251 145 150 155 160
252 Thr Pro Met Ser Ala Ala Arg Ala Leu Gly His His Phe Met Ala Ser
253 165 170 175
254 Leu Ile Thr Ala Glu Thr Cys Ala Lys Leu Glu Pro Glu Asp Ala Asp
255 180 185 190
256 Glu Asn Ile Asp Val Thr Ser Asn Asp Pro Glu Phe Pro Ser Ser Pro
257 195 200 205
258 Tyr Ser Ser Ser Ser Pro Cys Gly Leu Asp Ser Ile His Glu Thr Ser
259 210 215 220
260 Ala Arg Leu Leu Phe Met Ala Val Lys Trp Ala Lys Asn Leu Pro Val
261 225 230 235 240
262 Phe Ser Ser Leu Pro Phe Arg Asp Gln Val Pro Thr Gly Leu Pro Ala
263 245 250 255
264 Gly Glu Leu Gly Trp Ala Gly Val Arg Arg Pro Thr Arg Val Asn Gln

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FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/602,597

DATE: 12/04/2000

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Input Set : A:\472.app

Output Set: N:\CRF3\12042000\I602597.raw

L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

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